



## El Club Cuántico

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### NOTAS SOBRE EL CORONAVIRUS

Después de la epidemia provocada por el virus del SARS el año 2003 en China, para la comunidad científica resultaba claro que la emergencia de nuevos agentes infecciosos de similar naturaleza, potencialmente peligrosos para la humanidad, era inminente.

El año 2007, un artículo publicado en el *Clinical Microbiology Reviews* señalaba lo siguiente:

*The medical and scientific community demonstrated marvelous efforts in the understanding and control of SARS within a short time, as evident by over 4,000 publications available online. Despite these achievements, gaps still exist in terms of the molecular basis of the physical stability and transmissibility of this virus, the molecular and immunological basis of disease pathogenesis in humans, screening tests for early or cryptic SARS cases, foolproof infection control procedures for patient care, effective antivirals or antiviral combinations, the usefulness of immunomodulatory agents for late presenters, an effective vaccine with no immune enhancement, and the immediate animal host that transmitted the virus to caged civets in the market at the beginning of the epidemic. Coronaviruses are well known to undergo genetic recombination (375), which may lead to new genotypes and outbreaks. The presence of a large reservoir of SARS-CoV-like viruses in horseshoe bats, together with the culture of eating exotic mammals in southern China, is a time bomb. The possibility of the reemergence of SARS and other novel viruses from animals or laboratories and therefore the need for preparedness should not be ignored.*

**En el actual escenario, la probabilidad de que el SARS-CoV-2 fuese producto de manipulación en laboratorios queda prácticamente desechada, tal como se registra en una reciente publicación<sup>2</sup> (marzo de 2020):**

*It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus [...] Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used. However, the genetic data irrefutably show that SARSCoV-2 is not derived from any previously used virus backbone. Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer. We also discuss whether selection during passage could have given rise to SARS-CoV-2.*

Así, esta pandemia no era ni un evento imprevisible (mucho menos un oscuro complot o un fatal sino escrito en piedra), ni uno para el cual no hubiésemos tenido tiempo, como sociedad, para tomar precauciones y resguardos.

La ciencia, por si sola no dará soluciones a este tipo de problemas, si la sociedad misma no releva su importancia como actividad humana. De eso puede depender nuestra sobrevivencia como especie.

## Referencias

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